

gnl|CDD|8102, pfam01715, IPPT, IPP transferase. This is a family of IPP transferases EC:2.5.1.8 also known as tRNA delta(2)-isopentenylpyrophosphate transferase. These enzymes modify both cytoplasmic and mitochondrial tRNAs at A(37) to give isopentenyl A(37).

CD-Length = 253 residues, 90.5% aligned
Score = 173 bits (441), Expect = 3e-44

Query:	51	MQVYEGLDIITNKVSAQEQRICRHHMISFVDPLVTNYTVVDFRN RATALIEDIFARDKIP	110
Sbjct:	1	MQVYKGMDIGTAKPSLEEREGVPHHLIDILDPTES-Y SAAEFQRDALEAIAEIRARGKIP	59
Query:	111	IVVGGTNYYIESLLWKVLVNTKPQEMGTEKVIDRKVE--LEKEDGLVLHKRLSQVDPEMA	168
Sbjct:	60	LLVGGTGLYFKALLDGL----SDTPAADPKVRAKLEEQLEELGNDYLHAE LASVDPEAA	114
Query:	169	AKLHPHDKRKVARSLOVFEETGISHSEFLHRQHTEEGGGPLGGPLKFSNPCILWLHADQA	228
Sbjct:	115	AKIHPNDGRRIVRALEVFYATGKPISEFQKEQKNAL-----PYDIVQIGLARDRE	164
Query:	229	VLDERLDKRVDDMLAAGLLELRDFHRRYNQKNVSENSQDYQHGIFQSIGKFHEYLIT	288
Sbjct:	165	VLHERIARRVDDMLESGLVEEVKALYAQGLNEDL-----PSIRAIKYKEFLLYL--	213
Query:	289	EGKCTLETSNQLLKKG	304
Sbjct:	214	DGECTLEEAIERIIKN	229

gnl|CDD|405, smart00451, ZnF_U1, U1-like zinc finger; Family of C2H2-type zinc fingers, present in matrin, U1 small nuclear ribonucleoprotein C and other RNA-binding proteins.

CD-Length = 35 residues, 91.4% aligned
Score = 37.1 bits (86), Expect = 0.004

Query:	363	HLCDLCDRIIIDREWAHIIKS KSHLNQLKKR	394
Sbjct:	4	FYCKLCNVFTDEISVEAHLGKHHKKNVKKR	35

gnl|CDD|8115, pfam01745, IPT, Isopentenyl transferase. Isopentenyl transferase / dimethylallyl transferase synthesises isopentenyladenosine 5'-monophosphate, a cytokinin that induces shoot formation on host plants infected with the Ti plasmid.

CD-Length = 233 residues, only 16.7% aligned
Score = 36.8 bits (85), Expect = 0.005

Query:	19	LVVILGATGTGKSTLALQLGQRLGGEIVSADSMQVY EGL	57
Sbjct:	3	LYLIWGATCTGKTAEAIALAKSTGWPVIVLDRVQCCSQL	41

gnl|CDD|10515, COG0645, COG0645, Predicted kinase [General function prediction only]

CD-Length = 170 residues, only 18.2% aligned
Score = 36.5 bits (84), Expect = 0.007

Query:	19	LVVILGATGTGKSTLALQLGQRLGGEIVSAD	49
Sbjct:	3	LVLVGGLPGSGKSTLARGLAELLGAIRLSD	33

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L4 ANSWER 5 OF 6 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 2001:784384 SCISEARCH
THE GENUINE ARTICLE: 476WV
TITLE: Regulation of physiological rates in *Caenorhabditis elegans* by a tRNA-modifying enzyme in the mitochondria
AUTHOR: Lemieux J; Lakowski B; Webb A; Meng Y; Ubach A; Bussiere F; Barnes T; Hekimi S (Reprint)
CORPORATE SOURCE: McGill Univ, Dept Biol, 1205 Doctor Penfield Ave, Montreal, PQ H3A 1B1, Canada (Reprint); McGill Univ, Dept Biol, Montreal, PQ H3A 1B1, Canada
COUNTRY OF AUTHOR: Canada
SOURCE: GENETICS, (SEP 2001) Vol. 159, No. 1, pp. 147-157.
Publisher: GENETICS, 428 EAST PRESTON ST, BALTIMORE, MD 21202 USA.
ISSN: 0016-6731.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 39

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We show that the phenotype associated with *gro-1(e2400)* comprises the whole suite of features that characterize the phenotype of the *dl* mutants in *Caenorhabditis elegans*, including deregulated developmental, behavioral, and reproductive rates, as well as increased life span and a maternal effect. We cloned *gro-1* and found that it encodes a highly conserved cellular enzyme, isopentenylpyroptiosphate:tRNA transferase (IPT), which modifies a subset of tRNAs. In yeast, two forms of the enzyme are produced by alternative translation initiation, oric of which is mitochondrial. In the *gro-1* transcript there are also two possible initiator ATGs, between which there is a sequence predicted to encode a mitochondrial localization signal. A functional GRO-1::GFP fusion protein is localized diffusely throughout the cytoplasm and nucleus. A GRO-1::GFP initiated from the first methionine is localized exclusively to the mitochondria and rescues the mutant phenotype. In contrast, a protein initiated from the second methionine is localized diffusely throughout the cell and does not rescue the mutant phenotype. As oxygen consumption and ATP concentration have been reported to be unaffected in *gro-1* mutants, our observations suggest that GRO-1 acts in mitochondria and regulates global physiology by unknown mechanisms.

L4 ANSWER 2 OF 6 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 2002:441430 SCISEARCH
THE GENUINE ARTICLE: 552EV
TITLE: Allelic polymorphisms in the Fc gamma RIIC gene can influence its function on normal human natural killer cells
AUTHOR: Ernst L K; Metes D; Herberman R B; Morel P A (Reprint)
CORPORATE SOURCE: Univ Pittsburgh, Inst Canc, Pittsburgh, PA USA (Reprint); Univ Pittsburgh, Dept Pathol, Pittsburgh, PA USA; Univ Pittsburgh, Dept Surg, Pittsburgh, PA USA; Univ Pittsburgh, Dept Med, Pittsburgh, PA USA; Univ Pittsburgh,
COUNTRY OF AUTHOR: Dept Mol Genet & Biochem, Pittsburgh, PA USA
USA
SOURCE: JOURNAL OF MOLECULAR MEDICINE-JMM, (APR 2002) Vol. 80,
No. 4, pp. 248-257.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 31
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Natural killer (NK) cells are important in host defense against viruses and tumors and can induce death of virally infected cells following engagement of cell surface receptors. Human NK cells express receptors for the Fc portion of IgG which stimulate antibody-dependent cell-mediated cytotoxicity and induce cytokine production. We have shown that NK cells from certain individuals can express, in addition to CD16 (FcgammaRIIIa), isoforms of CD32 (FcgammaRIIc 1-4). Expression of CD32 on NK cells is dependent on an allelic polymorphism of the FcgammaRIIC gene. We analyzed the expression and function of CD32 on NK cells from 31 normal donors. Fourteen of the 31 (45%) donors expressed CD32 on their NK cells. Molecular characterization of FcgammaRIIc isoforms expressed by the CD32(+) donors revealed that the majority of donors expressed the FcgammaRIIc 1 isoform. Interestingly, 3 of the 14 positive donors did not express FcgammaRIIc 1, and we identified a novel isoform, FcgammaRIIc5, expressed by these individuals. The expression of this isoform was correlated to a second allelic polymorphism that controls exon splicing. One of the three was found to express FcgammaRIIb on the NK cells. Biochemical analysis revealed that CD32(+) donors of both types expressed a 40-kDa protein, specifically immunoprecipitated by anti-CD32 monoclonal antibodies. Functionally, only individuals expressing the FcgammaRIIc 1 isoform were able to trigger reverse antibody-dependent cell-mediated cytotoxicity via CD32 whereas a CD32(+) individual expressing the FcgammaRIIb isoform was unable to trigger this function. These results demonstrate that the presence of multiple allelic polymorphisms in the FcgammaRIIC gene determine the expression and function of CD32 on NK cells.



NCBI Conserved Domain Search

PubMed

Nucleotide

Protein

Structure

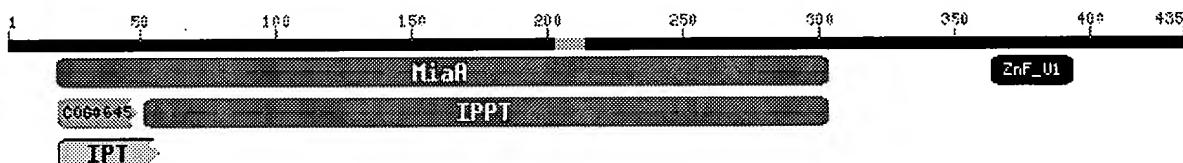
Taxonomy

RPS-BLAST 2.2.6 [Apr-09-2003]

Query= lcl|tmpseq_0
(435 letters)

Database: cdd.v1.62
11,088 PSSMs; 2,717,223 total columns

Click on boxes for multiple alignments



Show Domain Relatives

PSSMs producing significant alignments:	Score (bits)	E value
gnl CDD 10198 COG0324, MiaA, tRNA delta(2)-isopentenylpyrophosphate transfer...	226	5e-60

PSSMs producing significant alignments:	Score (bits)	E value
gnl CDD 10198 COG0324, MiaA, tRNA delta(2)-isopentenylpyrophosphate transfer...	226	5e-60
gnl CDD 8102 pfam01715, IPPT, IPP transferase. This is a family of IPP tran...	173	3e-44
gnl CDD 405 smart00451, ZnF_U1, U1-like zinc finger; Family of C2H2-type z...	37.1	0.004
gnl CDD 8115 pfam01745, IPT, Isopentenyl transferase. Isopentenyl transfera...	36.8	0.005
gnl CDD 10515 COG0645, COG0645, Predicted kinase [General function predictio...	36.5	0.007

gnl|CDD|10198, COG0324, MiaA, tRNA delta(2)-isopentenylpyrophosphate transferase [Translation, ribosomal structure and biogenesis]

CD-Length = 308 residues, 85.4% aligned
Score = 226 bits (577), Expect = 5e-60

Query: 18	PLVVILGATGTGKSTLALQLGQRLGGEIVSADSMQVYEGLDIITNKVSAQEQRICRHMI	77
Sbjct: 4	KLIVIAGPTASGKTALAIALAKRLGGEIISLDSMQVYRGLDIGTAKPSLEELAGVPHHLI	63
Query: 78	SFVDPLVTNYTVVDFRNRATALIEDIFARDKIPIVVGGTNYYIESLLWKVLVNTKPQEMG	137
Sbjct: 64	DIRDP-TESYSAAEFQRDALAAIDDILARGKLPILVGGTGLYLKA-LLEGLSLPPEADPE	121
Query: 138	TEKVIDRKVELEKEDGLVLHKRLSQVDPEMAAKLHPHDKRKVARSILQVFEETGISHSEFL	197
Sbjct: 122	VRRRLA--ELAELGNDALHAELKKIDPEAAAKIHPNDPQRIIRALEVYYLTGKPISELQ	179
Query: 198	HRQHTEEGGGPLGGPLKFNSNPCILWLHADQAVLDERLDKRVDDMLAAGLLEELRDFHRRY	257
Sbjct: 180	KRSRPILEPY-----DILIIALAADREVLYERINRRVDAMLEQGLIEEVKALYARG	230
Query: 258	NQKNVSENSQDYQHGIFQSIGFKEFHEYLITEGKCTLETSNQLKKG	304
Sbjct: 231	LHLD-----LPAMQAIGYKEILAYL--DGGISLEEAIERIKTA	266